

#30/jmu
09-19-01
1752

RAW SEQUENCE LISTING
PATENT APPLICATION: US/08/403,803A

DATE: 07/20/2001
TIME: 13:26:03

Input Set : A:\41426-A-PCT-US.txt
Output Set: N:\CRF3\07202001\H403803A.raw

3 <110> APPLICANT: Ron S. Israeli et al.
5 <120> TITLE OF INVENTION: PROSTATE-SPECIFIC MEMBRANE ANTIGEN
7 <130> FILE REFERENCE: 1769/41426-C/JPW/SHS
C--> 9 <140> CURRENT APPLICATION NUMBER: US/08/403,803A
C--> 9 <141> CURRENT FILING DATE: 1999-10-26
9 <160> NUMBER OF SEQ ID NOS: 38
11 <170> SOFTWARE: PatentIn version 3.0
13 <210> SEQ ID NO: 1
14 <211> LENGTH: 2653
15 <212> TYPE: DNA
16 <213> ORGANISM: human
18 <400> SEQUENCE: 1

Does Not
Corrected
See Ad

Does Not Comply
Corrected Diskette Needed
see Add 1 & Add 2

18 <400> SEQUENCE: 1
19 ctc当地
21 attggttcag tgc当地
23 gcg
25 cccg
27 cccg
29 acc
31 ctc
33 ccaa
35 ttatataatt
37 aag
39 gat
41 gat
43 gtt
45 ctag
47 atcaatt
49 gtt
51 tactt
53 cag
55 gca
57 gtt
59 ccacc
61 act
63 aga
65 ctgg
67 gtt
69 aga
71 tgg
73 tcat
75 gtac
77 tat
79 aaatt
81 agac
83 agt
85 ctc
87 cct
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Input Set : A:\41426-A-PCT-US.txt
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89	atttctatga	aacatccaca	ggaaaatgaag	acatacagtg	tatcatttga	ttcaactttt	2160									
91	tctgcagtaa	agaattttac	agaaaattgt	tccaaatc	gtgagagact	ccaggacttt	2220									
93	gacaaaagca	acccaatagt	attaagaatg	atgaatgatc	aactcatgtt	tctggaaaga	2280									
95	gcatttttg	atccatttagg	gttaccagac	aggcctttt	ataggcatgt	catctatgt	2340									
97	ccaaggcgc	acaacaagta	tgcaggggag	tcattcccag	gaatttatga	tgctctgtt	2400									
99	gatattgaaa	gcaaagtgg	cccttccaag	gcctggggag	aagtgaagag	acagatttat	2460									
101	gttgcagect	tcacagtgc	ggcagctgc	gagactttga	gtgaagtgc	ctaagaggat	2520									
103	tcttagaga	atccgtattt	aatttgtgt	gtatgtact	cagaaagaat	cgtaatgggt	2580									
105	atattgataa	attttaaaat	tggtatattt	gaaataaaat	tgaatattat	atataaaaaaa	2640									
107	aaaaaaaaaa	aaa					2653									
110	<210> SEQ ID NO: 2															
111	<211> LENGTH: 750															
112	<212> TYPE: PRT															
113	<213> ORGANISM: human															
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118	1			5			10									15
120	Arg	Pro	Arg	Trp	Leu	Cys	Ala	Gly	Ala	Leu	Val	Leu	Ala	Gly	Gly	Phe
121					20			25								30
123	Phe	Leu	Leu	Gly	Phe	Leu	Phe	Gly	Trp	Phe	Ile	Lys	Ser	Ser	Asn	Glu
124						35		40								45
126	Ala	Thr	Asn	Ile	Thr	Pro	Lys	His	Asn	Met	Lys	Ala	Phe	Leu	Asp	Glu
127						50		55								60
129	Leu	Lys	Ala	Glu	Asn	Ile	Lys	Lys	Phe	Leu	Tyr	Asn	Phe	Thr	Gln	Ile
130						65		70								80
132	Pro	His	Leu	Ala	Gly	Thr	Glu	Gln	Asn	Phe	Gln	Leu	Ala	Lys	Gln	Ile
133						85		90								95
135	Gln	Ser	Gln	Trp	Lys	Glu	Phe	Gly	Leu	Asp	Ser	Val	Glu	Leu	Ala	His
136						100		105								110
138	Tyr	Asp	Val	Leu	Leu	Ser	Tyr	Pro	Asn	Lys	Thr	His	Pro	Asn	Tyr	Ile
139						115		120								125
141	Ser	Ile	Ile	Asn	Glu	Asp	Gly	Asn	Glu	Ile	Phe	Asn	Thr	Ser	Leu	Phe
142						130		135								140
144	Glu	Pro	Pro	Pro	Gly	Tyr	Glu	Asn	Val	Ser	Asp	Ile	Val	Pro	Pro	
145						145		150								160
147	Phe	Ser	Ala	Phe	Ser	Pro	Gln	Gly	Met	Pro	Glu	Gly	Asp	Leu	Val	Tyr
148						165		170								175
150	Val	Asn	Tyr	Ala	Arg	Thr	Glu	Asp	Phe	Phe	Lys	Leu	Glu	Arg	Asp	Met
151						180		185								190
153	Lys	Ile	Asn	Cys	Ser	Gly	Lys	Ile	Val	Ile	Ala	Arg	Tyr	Gly	Lys	Val
154						195		200								205
156	Phe	Arg	Gly	Asn	Lys	Val	Lys	Asn	Ala	Gln	Leu	Ala	Gly	Ala	Lys	Gly
157						210		215								220
159	Val	Ile	Leu	Tyr	Ser	Asp	Pro	Ala	Asp	Tyr	Phe	Ala	Pro	Gly	Val	Lys
160						225		230								240
162	Ser	Tyr	Pro	Asp	Gly	Trp	Asn	Leu	Pro	Gly	Gly	Gly	Val	Gln	Arg	Gly
163						245		250								255
165	Asn	Ile	Leu	Asn	Leu	Asn	Gly	Ala	Gly	Asp	Pro	Leu	Thr	Pro	Gly	Tyr
166						260		265								270

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Input Set : A:\41426-A-PCT-US.txt
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168 Pro Ala Asn Glu Tyr Ala Tyr Arg Arg Gly Ile Ala Glu Ala Val Gly
169 275 280 285
171 Leu Pro Ser Ile Pro Val His Pro Ile Gly Tyr Tyr Asp Ala Gln Lys
172 290 295 300
174 Leu Leu Glu Lys Met Gly Gly Ser Ala Pro Pro Asp Ser Ser Trp Arg
175 305 310 315 320
177 Gly Ser Leu Lys Val Pro Tyr Asn Val Gly Pro Gly Phe Thr Gly Asn
178 325 330 335
180 Phe Ser Thr Gln Lys Val Lys Met His Ile His Ser Thr Asn Glu Val
181 340 345 350
183 Thr Arg Ile Tyr Asn Val Ile Gly Thr Leu Arg Gly Ala Val Glu Pro
184 355 360 365
186 Asp Arg Tyr Val Ile Leu Gly Gly His Arg Asp Ser Trp Val Phe Gly
187 370 375 380
189 Gly Ile Asp Pro Gln Ser Gly Ala Ala Val Val His Glu Ile Val Arg
190 385 390 395 400
192 Ser Phe Gly Thr Leu Lys Lys Glu Gly Trp Arg Pro Arg Arg Thr Ile
193 405 410 415
195 Leu Phe Ala Ser Trp Asp Ala Glu Glu Phe Gly Leu Leu Gly Ser Thr
196 420 425 430
198 Glu Trp Ala Glu Glu Asn Ser Arg Leu Leu Gln Glu Arg Gly Val Ala
199 435 440 445
201 Tyr Ile Asn Ala Asp Ser Ser Ile Glu Gly Asn Tyr Thr Leu Arg Val
202 450 455 460
204 Asp Cys Thr Pro Leu Met Tyr Ser Leu Val His Asn Leu Thr Lys Glu
205 465 470 475 480
207 Leu Lys Ser Pro Asp Glu Gly Phe Glu Gly Lys Ser Leu Tyr Glu Ser
208 485 490 495
210 Trp Thr Lys Lys Ser Pro Ser Pro Glu Phe Ser Gly Met Pro Arg Ile
211 500 505 510
213 Ser Lys Leu Gly Ser Gly Asn Asp Phe Glu Val Phe Phe Gln Arg Leu
214 515 520 525
216 Lys Ile Ala Ser Gly Arg Ala Arg Tyr Thr Lys Asn Trp Glu Thr Asn
217 530 535 540
219 Lys Phe Ser Gly Tyr Pro Leu Tyr His Ser Val Tyr Glu Thr Tyr Glu
220 545 550 555 560
222 Leu Val Glu Lys Phe Tyr Asp Pro Met Phe Lys Tyr His Leu Thr Val
223 565 570 575
225 Ala Gln Val Arg Gly Gly Met Val Phe Glu Leu Ala Asn Ser Ile Val
226 580 585 590
228 Leu Pro Phe Asp Cys Arg Asp Tyr Ala Val Val Leu Arg Lys Tyr Ala
229 595 600 605
231 Asp Lys Ile Tyr Ser Ile Ser Met Lys His Pro Gln Glu Met Lys Thr
232 610 615 620
234 Tyr Ser Val Ser Phe Asp Ser Leu Phe Ser Ala Val Lys Asn Phe Thr
235 625 630 635 640
237 Glu Ile Ala Ser Lys Phe Ser Glu Arg Leu Gln Asp Phe Asp Lys Ser
238 645 650 655
240 Asn Pro Ile Val Leu Arg Met Met Asn Asp Gln Leu Met Phe Leu Glu

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Input Set : A:\41426-A-PCT-US.txt
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241 660 665 670
 243 Arg Ala Phe Ile Asp Pro Leu Gly Leu Pro Asp Arg Pro Phe Tyr Arg
 244 675 680 685
 246 His Val Ile Tyr Ala Pro Ser Ser His Asn Lys Tyr Ala Gly Glu Ser
 247 690 695 700
 249 Phe Pro Gly Ile Tyr Asp Ala Leu Phe Asp Ile Glu Ser Lys Val Asp
 250 705 710 715 720
 252 Pro Ser Lys Ala Trp Gly Glu Val Lys Arg Gln Ile Tyr Val Ala Ala
 253 725 730 735
 255 Phe Thr Val Gln Ala Ala Ala Glu Thr Leu Ser Glu Val Ala
 256 740 745 750
 258 <210> SEQ ID NO: 3
 259 <211> LENGTH: 8
 260 <212> TYPE: PRT
 261 <213> ORGANISM: human
 263 <400> SEQUENCE: 3
 265 Ser Leu Tyr Glu Ser Trp Thr Lys
 266 1 5
 268 <210> SEQ ID NO: 4
 269 <211> LENGTH: 15
 270 <212> TYPE: PRT
 271 <213> ORGANISM: human
 273 <220> FEATURE:
 W--> 274 <221> NAME/KEY: misc.
 275 <222> LOCATION: (1)..(15)
 276 <223> OTHER INFORMATION: x=unknown
 279 <400> SEQUENCE: 4
 W--> 281 Ser Tyr Pro Asp Gly Xaa Xaa Leu Pro Gly Gly Val Gln Arg
 282 1 5 10 15
 284 <210> SEQ ID NO: 5
 285 <211> LENGTH: 7
 286 <212> TYPE: PRT
 287 <213> ORGANISM: human
 289 <400> SEQUENCE: 5
 291 Phe Tyr Asp Pro Met Phe Lys
 292 1 5
 294 <210> SEQ ID NO: 6
 295 <211> LENGTH: 9
 296 <212> TYPE: PRT
 297 <213> ORGANISM: human
 299 <400> SEQUENCE: 6
 301 Ile Tyr Asn Val Ile Gly Thr Leu Lys
 302 1 5
 304 <210> SEQ ID NO: 7
 305 <211> LENGTH: 22
 306 <212> TYPE: PRT
 307 <213> ORGANISM: human
 309 <220> FEATURE:
 W--> 310 <221> NAME/KEY: misc

RAW SEQUENCE LISTING DATE: 07/20/2001
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Input Set : A:\41426-A-PCT-US.txt
 Output Set: N:\CRF3\07202001\H403803A.raw

311 <222> LOCATION: (1)..(22)
 312 <223> OTHER INFORMATION: x=unknown
 315 <400> SEQUENCE: 7
 W--> 317 Phe Leu Tyr Xaa Xaa Thr Gln Ile Pro His Leu Ala Gly Thr Glu Gln
 318 1 5 10 15
 320 Asn Phe Gln Leu Ala Lys
 321 20
 323 <210> SEQ ID NO: 8
 324 <211> LENGTH: 17
 325 <212> TYPE: PRT
 326 <213> ORGANISM: human
 328 <400> SEQUENCE: 8
 330 Gly Val Ile Leu Tyr Ser Asp Pro Ala Asp Tyr Phe Ala Pro Asp Val
 331 1 5 10 15
 333 Lys
 336 <210> SEQ ID NO: 9
 337 <211> LENGTH: 17
 338 <212> TYPE: PRT
 339 <213> ORGANISM: human
 341 <400> SEQUENCE: 9
 343 Pro Val Ile Leu Tyr Ser Asp Pro Ala Asp Tyr Phe Ala Pro Gly Val
 344 1 5 10 15
 346 Lys
 349 <210> SEQ ID NO: 10
 350 <211> LENGTH: 15
 351 <212> TYPE: PRT
 352 <213> ORGANISM: human
 354 <400> SEQUENCE: 10
 356 Ala Phe Ile Asp Pro Leu Gly Leu Pro Asp Arg Pro Phe Tyr Arg
 357 1 5 10 15
 359 <210> SEQ ID NO: 11
 360 <211> LENGTH: 19
 361 <212> TYPE: PRT
 362 <213> ORGANISM: human
 364 <400> SEQUENCE: 11
 366 Tyr Ala Gly Glu Ser Phe Pro Gly Ile Tyr Asp Ala Leu Phe Asp Ile
 367 1 5 10 15
 369 Glu Ser Lys
 372 <210> SEQ ID NO: 12
 373 <211> LENGTH: 22
 374 <212> TYPE: PRT
 375 <213> ORGANISM: human
 377 <220> FEATURE:
 W--> 378 <221> NAME/KEY: misc.
 379 <222> LOCATION: (1)..(22)
 380 <223> OTHER INFORMATION: x=unknown
 383 <400> SEQUENCE: 12
 W--> 385 Thr Ile Leu Phe Ala Ser Trp Asp Ala Glu Glu Phe Gly Xaa Xaa Gly
 386 1 5 10 15
 Fyt,

Use of 'n' and/or 'Xaa' has been detected in the Sequence Listing. Review the Sequence Listing to insure a corresponding explanation is presented in the <220> to <223> fields of each sequence using 'n' or 'Xaa'.

Add1

<210> 13

<211> 17

<212> DNA

<213> artificial;primer

<220>

<221> misc.

<222> (1)..(16)

<223> n=unknown

<400> 13

ttyaygayc cnatgtt

17

sec item # 10 on
ERROR summary

Sheet
↓

The type of errors shown exist throughout
the Sequence Listing. Please check subsequent
sequences for similar errors.

<210> 14

<211> 17

<212> DNA

<213> artificial;primer

<220>

<221> misc

<222> (1)..(16)

<223> n=unknown

<400> 14

aacatnggrt crtaraa

17

<210> 15

<211> 17

<212> DNA

<213> artificial;primer

<220>

<221> misc.

Add 2

<210> 30

<211> 27

<212> DNA

<213> artificial

see item # 11 on ERROR
Summary SHEET.

<400> 30

acggagcaaa actttcagct tgcaaag

27

VERIFICATION SUMMARY DATE: 07/20/2001
 PATENT APPLICATION: US/08/403,803A TIME: 13:26:04

Input Set : A:\41426-A-PCT-US.txt
 Output Set: N:\CRF3\07202001\H403803A.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application No
 L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date
 L:274 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
 L:281 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
 L:310 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:7
 L:317 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
 L:378 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:12
 L:385 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
 L:394 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:13
 L:397 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:13
 L:403 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
 L:409 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:14
 L:412 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:14
 L:418 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
 L:424 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:15
 L:427 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:15
 L:433 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
 L:439 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:16
 L:442 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:16
 L:448 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
 L:454 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:17
 L:457 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:17
 L:463 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
 L:469 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:18
 L:472 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:18
 L:478 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
 L:484 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:19
 L:487 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:19
 L:493 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19
 L:499 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:20
 L:502 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:20
 L:508 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
 L:514 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:21
 L:516 M:258 W: Mandatory Feature missing, <220> FEATURE:
 L:516 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
 L:523 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:22
 L:525 M:258 W: Mandatory Feature missing, <220> FEATURE:
 L:525 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
 L:532 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:23
 L:535 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:23
 L:541 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
 L:547 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:24
 L:550 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:24
 L:556 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24
 L:562 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:25
 L:565 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:25
 L:571 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
 L:577 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:26

VERIFICATION SUMMARY
PATENT APPLICATION: US/08/403,803A

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Input Set : A:\41426-A-PCT-US.txt
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L:580 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:586 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
L:595 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:27
L:603 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:607 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:609 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:619 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:621 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:625 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:634 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:28
L:646 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:648 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:652 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:654 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:656 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:658 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:669 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:29
L:681 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29
L:687 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29
L:697 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:30
L:699 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:699 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:706 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:31
L:708 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:708 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:716 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:32
L:718 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:718 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:725 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:33
L:727 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:727 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:734 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:34
L:736 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:736 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:

RECEIVED

SEP 11 2001

Raw Sequence Listing Error Summary

TECH CENTER 1600/2900

ERROR DETECTED SUGGESTED CORRECTION SERIAL NUMBER: 08/403,803A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 Wrapped Nucleic
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use **space characters**, instead.

4 Non-ASCII The submitted file was **not** saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

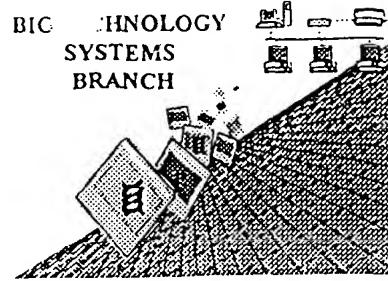
8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence

11 Use of <220>
 30 Sequence(s) 30 missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 PatentIn 2.0
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